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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/591,271	08/06/2007	Christopher T. Harbison	WTHD-002	5936

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EXAMINER	
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ART UNIT	PAPER NUMBER
1634	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/591,271	HARBISON ET AL.	
	Examiner	Art Unit	
	Ethan Whisenant	1634	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3* MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *17 December 2008*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-3,7,8,12,16,17,19,24,26,28,36,38,41,45-48 and 60* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☒ Claim(s) *60* is/are allowed.

6)☒ Claim(s) *1-3,7,8,12,16,17,19,24,26,28,38,41,45,46 and 48* is/are rejected.

7)☒ Claim(s) *7,36 and 47* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *31 August 2006* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

NON-FINAL ACTION

1. The applicant's response (filed 17 DEC 08) to the Office Action has been entered. Following the entry of the claim amendment(s), **Claim(s) 1-3, 7-8, 12, 16-17, 19, 24, 26, 28, 36, 38, 41, 45-48 and 60** is/are pending. Rejections and/or objections not reiterated from the previous office action are hereby withdrawn. The following rejections and/or objections are either newly applied or reiterated. They constitute the complete set presently being applied to the instant application.

35 USC § 112- 2nd Paragraph

2. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

CLAIM REJECTIONS under 35 USC § 112- 2ND PARAGRAPH

3. **Claim(s) 45-46 and 48** is/are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 45 is indefinite because there is no nexus between the preamble and the claim steps. Claim 45 in its preamble direct to a method which is to accomplish a particular goal. However, none of the claim steps states that this goal is accomplished. For clarity, claimed methods should recite that the purpose of the method has been attained (i.e. provide a nexus between the preamble and the claim steps).

35 USC § 102

4. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that may form the basis for rejections set forth in this Office action:

> A person shall be entitled to a patent unless --
>
> **(a)** the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> **(b)** the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> **(e)** the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.
> or
> **(e)** the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

CLAIM REJECTIONS UNDER 35 USC § 102

5. **Claim(s) 1-3, 8, 12, 16-17, 19, 24, 26, 28** is/are rejected under 35 U.S.C. 102(a) as being anticipated by Wang et al. [Bioinformatics 19(18) : 2369-2380 (DEC 2003)].

Claim 1 is drawn to a method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell which method comprises three steps. To begin, a set of regions of genomic DNA to which the protein of interest is bound is identified. Next, candidate DNA-binding sites in the identified regions of genomic DNA are identified, wherein a candidate DNA-binding site comprises a sequence corresponding to a DNA-sequence motif for the protein of interest. Finally it is determined if the candidate DNA-binding sites are conserved in an equivalent genomic region in one or more species different from the species from which the cell is obtained, wherein a candidate DNA-binding site

that is conserved in at least one of the different species is a biologically-active DNA-binding site.

Wang et al. teach a method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell which comprises the required three steps of Claim 1, see for example Figure 1.

Claim 2 is drawn to an embodiment of the method of Claim 1 wherein step (i) further comprises identifying a DNA sequence motif for the protein from the set of regions of genomic DNA.

Wang et al. teach this limitation. See the panel at the bottom of Figure 1 which is entitled "Results of profile comparison".

Claim 3 is drawn to an embodiment of the method of Claim 2 wherein the DNA sequence motif is enriched by a statistically-significant amount in the set of regions of genomic DNA relative to a suitable control.

Wang et al. teach this limitation. See the portion of the "Results" section entitled "Scoring statistics" on p. 2373.

Claim 8 is drawn to an embodiment of the method of Claim 1 wherein the regions of genomic DNA comprise promoter regions.

Wang et al. teach this limitation. See the portion of the paragraph bridging columns 1 and 2 on p.2370.

Claim 12 is drawn to an embodiment of the method of Claim 2 wherein a candidate DNA-binding site is conserved if the equivalent genomic region in at least one different species comprises a nucleic acid sequence that matches the DNA-sequence motif for the protein of interest.

Wang et al. teach this limitation, see for example Figure 1.

Claim 16 is drawn to an embodiment of the method of Claim 1 wherein the candidate DNA-binding site is less than 20 bp in length.

Wang et al. teach this limitation, see, for example Figure 1 and Tables 1 and 2.

Claim 17 is drawn to an embodiment of the method of Claim 1 wherein the DNA –sequence motif is degenerate in at least one position.

Wang et al. teach this limitation, see, for example Figure 1 and Tables 1 and 2.

Claim 19 is drawn to an embodiment of the method of Claim 1 wherein the step (iii) comprises determining if the candidate DNA-binding sites are conserved in equivalent genomic regions in two or more different species.

Wang et al. teach this limitation, see, for example Figure 1.

Claim 24 is drawn to an embodiment of the method of Claim 1 wherein the set of biologically-active DNA-binding sites comprises one or more biologically-active DNA-binding sites.

Wang et al. teach this limitation, see, for example Figure 1.

Claim 26 is drawn to an embodiment of the method of Claim 1 wherein two regions of genomic DNA are equivalent if they both comprise a sequence of at least one orthologous gene.

Wang et al. teach this limitation, see, for example Figure 1.

Claim 28 is drawn to an embodiment of the method of Claim 1 wherein the cell is an eukaryotic cell.

Wang et al. teach this limitation in that the DNA sequences analyzed are from yeast (i.e. organisms comprising eukaryotic-type cell structure).

6. Claim(s) 1-3, 8, 12, 16-17, 19, 24, 26, 28, 38 and 41 is/are rejected under 35 U.S.C. 102(a) as being anticipated by Kellis et al. [Nature 423 : 241-254 (MAY 2003)].

Claim 1 is drawn to a method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell which method comprises three steps. To begin, a set of regions of genomic DNA to which the protein of interest is bound is identified. Next, candidate DNA-binding sites in the identified regions of genomic DNA are identified, wherein a candidate DNA-binding site comprises a sequence corresponding to a DNA-sequence motif for the protein of interest. Finally it is determined if the candidate DNA-binding sites are conserved in an equivalent genomic region in one or more species different from the species from which the cell is obtained, wherein a candidate DNA-binding site that is conserved in at least one of the different species is a biologically-active DNA-binding site.

Kellis et al. teach a method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell which comprises the three steps recited in Claim 1, see for example p. 247- beginning at the section entitled “Genome-wide identification of regulatory elements” to end of the “Disscussion” section on p. 253

Claim 2 is drawn to an embodiment of the method of Claim 1 wherein step (i) further comprises identifying a DNA sequence motif for the protein from the set of regions of genomic DNA.

Kellis et al. teach this limitation. See Tables 2-4.

Claim 3 is drawn to an embodiment of the method of Claim 2 wherein the DNA sequence motif is enriched by a statistically-significant amount in the set of regions of genomic DNA relative to a suitable control.

Kellis et al. teach this limitation. See the section entitled "Methodology for genome-wide motif discovery" which begins on p. 248.

Claim 8 is drawn to an embodiment of the method of Claim 1 wherein the regions of genomic DNA comprise promoter regions.

Kellis et al. teach this limitation, see the section entitled "Genome-wide identification of regulatory elements" on p. 247

Claim 12 is drawn to an embodiment of the method of Claim 2 wherein a candidate DNA-binding site is conserved if the equivalent genomic region in at least one different species comprises a nucleic acid sequence that matches the DNA-sequence motif for the protein of interest.

Kellis et al. teach this limitation, see for example Figure 6.

Claim 16 is drawn to an embodiment of the method of Claim 1 wherein the candidate DNA-binding site is less than 20 bp in length.

Kellis et al. teach this limitation, see, for example Figure 6 and Tables 2-4.

Claim 17 is drawn to an embodiment of the method of Claim 1 wherein the DNA –sequence motif is degenerate in at least one position.

Kellis et al. teach this limitation, see, for example Figure 6 and Tables 2-4.

Claim 19 is drawn to an embodiment of the method of Claim 1 wherein the step (iii) comprises determining if the candidate DNA-binding sites are conserved in equivalent genomic regions in two or more different species.

Kellis et al. teach this limitation, see, for example Figure 6 and Tables 2-4.

Claim 24 is drawn to an embodiment of the method of Claim 1 wherein the set of biologically-active DNA-binding sites comprises one or more biologically-active DNA-binding sites.

Kellis et al. teach this limitation, see, for example Figure 1.

Claim 26 is drawn to an embodiment of the method of Claim 1 wherein two regions of genomic DNA are equivalent if they both comprise a sequence of at least one orthologous gene.

Kellis et al. teach this limitation, see, for example Figure 1.

Claim 28 is drawn to an embodiment of the method of Claim 1 wherein the cell is an eukaryotic cell.

Kellis et al. teach this limitation in that the DNA sequences analyzed are from yeast (i.e. organisms comprising eukaryotic-type cell structure).

Claim 38 is drawn to a method of identifying a pathway that is transcriptionally regulated by a protein of interest in a cell the method comprising two steps. i) To begin, a set of biologically-active DNA-binding sites for a protein of interest in the genome of the cell are identified according to the method of claim 2; Next, at least two candidate genes likely to be regulated by binding of the protein of interest to the set of biologically-active DNA-binding sites identified in (i) wherein a pathway that is transcriptionally regulated by the protein of interest is identified if at least two candidate genes are members of the same pathway.

Kellis et al. teach a method of identifying a pathway that is transcriptionally regulated by a protein of interest in a cell, see the section entitled “Infering function of genome-wide motifs” which begins on p.250.

Claim 41 is drawn to an embodiment of the method of Claim 38 wherein the pathway is a gene expression pathway.

Kellis et al. teach this limitation wherein these authors teach analyzing the Gal4 motif and it association with carbohydrate metabolism (i.e. a gene expression pathway), see the section entitled "Infering function of genome-wide motifs" which begins on p.250.

7. Claim(s) 1-3, 8, 12, 16-17, 19, 24 and 26 is/are rejected under 35 U.S.C. 102(b) as being anticipated by McCue et al. [Nucleic Acids Research 29(3) : 774-782 (2001)].

Claim 1 is drawn to a method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell which method comprises three steps. To begin, a set of regions of genomic DNA to which the protein of interest is bound is identified. Next, candidate DNA-binding sites in the identified regions of genomic DNA are identified, wherein a candidate DNA-binding site comprises a sequence corresponding to a DNA-sequence motif for the protein of interest. Finally it is determined if the candidate DNA-binding sites are conserved in an equivalent genomic region in one or more species different from the species from which the cell is obtained, wherein a candidate DNA-binding site that is conserved in at least one of the different species is a biologically-active DNA-binding site.

McCue et al. teach a method of identifying a set of biologically-active DNA-binding sites for a protein of interest in the genome of a cell which comprises the three steps recited in Claim 1, see for example Figure 2 on p. 779

Claim 2 is drawn to an embodiment of the method of Claim 1 wherein step (i) further comprises identifying a DNA sequence motif for the protein from the set of regions of genomic DNA.

McCue et al. teach this limitation, see for example Figure 2 on p. 779.

Claim 3 is drawn to an embodiment of the method of Claim 2 wherein the DNA sequence motif is enriched by a statistically-significant amount in the set of regions of genomic DNA relative to a suitable control.

McCue et al. teach this limitation, see the section entitled "Bayesian Gibbs sampling" on p.775.

Claim 8 is drawn to an embodiment of the method of Claim 1 wherein the regions of genomic DNA comprise promoter regions.

McCue et al. teach this limitation, see the "Introduction" on p. 774.

Claim 12 is drawn to an embodiment of the method of Claim 2 wherein a candidate DNA-binding site is conserved if the equivalent genomic region in at least one different species comprises a nucleic acid sequence that matches the DNA-sequence motif for the protein of interest.

McCue et al. teach this limitation, see Figure 2.

Claim 16 is drawn to an embodiment of the method of Claim 1 wherein the candidate DNA-binding site is less than 20 bp in length.

McCue et al. teach this limitation, see Figure 2.

Claim 17 is drawn to an embodiment of the method of Claim 1 wherein the DNA –sequence motif is degenerate in at least one position.

McCue et al. teach this limitation, see Figure 2.

Claim 19 is drawn to an embodiment of the method of Claim 1 wherein the step (iii) comprises determining if the candidate DNA-binding sites are conserved in equivalent genomic regions in two or more different species.

McCue et al. teach this limitation, see Figure 2.

Claim 24 is drawn to an embodiment of the method of Claim 1 wherein the set of biologically-active DNA-binding sites comprises one or more biologically-active DNA-binding sites.

McCue et al. teach this limitation, see Figure 2.

Claim 26 is drawn to an embodiment of the method of Claim 1 wherein two regions of genomic DNA are equivalent if they both comprise a sequence of at least one orthologous gene.

McCue et al. teach this limitation, see Figure 2.

CLAIM OBJECTIONS

8. **Claim(s) 7, 36 and 47** is /are objected to as being dependent upon a rejected base claim, but would appear to be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

ALLOWABLE SUBJECT MATTER

9. **Claim(s) 45-46 and 48** would appear to be allowable if rewritten to overcome the rejection(s) under 35 U.S.C. 112 set forth in this Office action bacause the prior art of record, if considered individually, do not teach, or if considered in any combination, do not reasonably suggest the methods recited in Claims 45-46 and 48.

REASON FOR ALLOWANCE

10. **Claim 60** is allowable over the prior art of record. Independent Claim 60 is allowable over the prior art of record because none of the references of record alone teach all of the limitations recited in Claims 11, 16 or 23. Neither does the prior art of record, in any combination, reasonably suggest the method(s) recited in independent Claim 60.

CONCLUSION

11. **Claim(s) 60** is/are allowable while **Claim(s) 1-3, 7-8, 12, 16-17, 19, 24, 26, 28, 36, 38, 41 and 45-48** is/are rejected and/or objected to for the reason(s) set forth above.

12. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ethan Whisenant, Ph.D. whose telephone number is (571) 272-0754. The examiner can normally be reached Monday-Friday from 8:30AM - 5:30PM EST or any time via voice mail. If repeated attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ram Shukla, can be reached at (571) 272-0735.

The Central Fax number for the USPTO is (571) 273-8300. Please note that the faxing of papers must conform with the Notice to Comply published in the Official Gazette, 1096 OG 30 (November 15, 1989).

/Ethan Whisenant/
Primary Examiner
Art Unit 1634

EXAMINER SEARCH NOTES

06 MAR 09 - ECW

Databases searched: USPATFULL, USPG-PUBS, JAPIO and EUROPATFULL via EAST &

CAplus, Medline and BIOSIS via STN

Reviewed the parent(s), if any, and any search(es) performed therein : see the BIB data sheet

Reviewed, the search(es), if any, performed by prior examiners

Search terms:

Inventor(s) : e.g. Harbison C?/au

DNA binding site$

Protein binding Site$

Genomic DNA or DNA

Conserved or Conservation

Control$

Motif$

Orthologous

Eukaryot$

Promoter$

Transcription factor$

Genotype$

Mutant